



SEQUENCE LISTING

B11

<10> VETIGEN
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MOROOKA, Shigeaki

<120> MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS

<130> 053356-5001-US

<140> US 09/319,724

<141> 1999-09-08

<150> EP 96402719.7

<151> 1996-12-12

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 439

<212> PRT

<213> Homo sapiens

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Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu Glu Ile
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Gly Phe Asn Gly Asn Arg Ile Val Asp Val Asn Leu Thr Ser Glu Gly
35 40 45

Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val
50 55 60

Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr
65 70 75 80

Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe
85 90 95

Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile
100 105 110

Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu
 115 120 125
 Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys
 130 135 140
 Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe
 145 150 155 160
 Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile
 165 170 175
 Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser
 180 185 190
 Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn
 195 200 205
 Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp
 210 215 220
 Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys
 225 230 235 240
 Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser
 245 250 255
 Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe
 260 265 270
 Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn
 275 280 285
 Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg
 290 295 300
 Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys
 305 310 315 320
 Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe
 325 330 335

Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe
340 345 350

Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr
355 360 365

Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln
370 375 380

Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
385 390 395 400

Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
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Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu
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Gly Ile Met Cys Gly Ala Ile
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gatgttaatc taactagtga aggaaagggt aaactgggtc caaatactaa aatccagatg 180
tcatattcag taaaatggaa aaagtcagat gtgaaatttg aagatcgatt tgacaaatat 240
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tcctctctga ttggttctgg atgtcagata tttgctgtgt ctctcatcgt tattattggt 540
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tatgctgcta cgtctccagt gaatgggttat tttggaggaa gtctgtatgc tagacaagga 660
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p11

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ttcatgatgg tgatcttctt ggtgggctta gtttcaatga ttttaatgag aacattaaga 180
aaagattatg ctcggtacag taaagaggaa gaaatggatg atatggatag agacctagga 240
gatgaatatg gatggaaaca ggtgcatgga gatgtattta gaccatcaag tcacccactg 300
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tttgtctatg ctgctacgtc tccagtgaat ggttatatta gaggaagtct gtatgctaga 480
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gtttgcctgg gtggaatttt accttttggg tcaatcttta ttgaaatgta tttcatcttc 840
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Sub
C1
cont

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gaaga 965

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atcttcttgg tgggcttagt ttcaatgatt ttaatgagaa cattaagaaa agattatgct 180
cggtagagta aagagggaaga aatggatgat atggatagag acctaggaga tgaatatgga 240
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Ser

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<223> Xaa can be any amino acid

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His

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<212> DNA
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<223> probe/primer

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<220>
<223> probe/primer

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47

gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc tta tgg
Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp
20 25 30

95

atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat aag tac
Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr
35 40 45

143

ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt cat tac
Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr
50 55 60

191

cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt
His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser
65 70 75

239

ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act tac tgt 287
 Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys
 80 85 90 95

gaa att gat tta gat aaa gaa aag aga gat gca ttt gta tat gcc ata 335
 Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile
 100 105 110

aaa aat cat tac tgg tac cag atg tac ata gat gat tta cca ata tgg 383
 Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp
 115 120 125

ggt att gtt ggt gag gct gat gaa aat gga gaa gat tac tat ctt tgg 431
 Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp
 130 135 140

acc tat aaa aaa ctt gaa ata ggt ttt aat gga aat cga att gtt gat 479
 Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp
 145 150 155

gtt aat cta act agt gaa gga aag gtg aaa ctg gtt cca aat act aaa 527
 Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys
 160 165 170 175

atc cag atg tca tat tca gta aaa tgg aaa aag tca gat gtg aaa ttt 575
 Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe
 180 185 190

gaa gat cga ttt gac aaa tat ctt gat ccg tcc ttt ttt caa cat cgg 623
 Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg
 195 200 205

att cat tgg ttt tca att ttc aac tcc ttc atg atg gtg atc ttc ttg 671
 Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu
 210 215 220

gtg ggc tta gtt tca atg att tta atg aga aca tta aga aaa gat tat 719
 Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr
 225 230 235

gct cgg tac agt aaa gag gaa gaa atg gat gat atg gat aga gac cta 767
 Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu
 240 245 250 255

gga gat gaa tat gga tgg aaa cag gtg cat gga gat gta ttt aga cca 815
 Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro
 260 265 270

tca agt cac cca ctg ata ttt tcc tct ctg att ggt tct gga tgt cag 863
 Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln
 275 280 285

ata ttt gct gtg tct ctc atc gtt att att gtt gca atg ata gaa gat 911
 Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp
 290 295 300

tta tat act gag agg gga tca atg ctc agt aca gcc ata ttt gtc tat 959

Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr
 305 310 315
 gct gct acg tct cca gtg aat ggt tat ttt gga gga agt ctg tat gct 1007
 Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala
 320 325 330 335
 aga caa gga gga agg aga tgg ata aag cag atg ttt att ggg gca ttc 1055
 Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe
 340 345 350
 ctt atc cca gct atg gtg tgt ggc act gcc ttc ttc atc aat ttc ata 1103
 Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile
 355 360 365
 gcc att tat tac cat gct tca aga gcc att cct ttt gga aca atg gtg 1151
 Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val
 370 375 380
 gcc gtt tgt tgc atc tgt ttt ttt gtt att ctt cct cta aat ctt gtt 1199
 Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val
 385 390 395
 ggt aca ata ctt ggc cga aat ctg tca ggt cag ccc aac ttt cct tgt 1247
 Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys
 400 405 410 415
 cgt gtc aat gct gtg cct cgt cct ata ccg gag aaa aaa tgg ttc atg 1295
 Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met
 420 425 430
 gag cct gcg gtt att gtt tgc ctg ggt gga att tta cct ttt ggt tca 1343
 Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser
 435 440 445
 atc ttt att gaa atg tat ttc atc ttc acg tct ttc tgg gca tat aag 1391
 Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys
 450 455 460
 atc tat tat gtc tat ggc ttc atg atg ctg gtg ctg gtt atc ctg tgc 1439
 Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys
 465 470 475
 att gtg act gtc tgt gtg act att gtg tgc aca tat ttt cta cta aat 1487
 Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn
 480 485 490 495
 gca gaa gat tac cgg tgg caa tgg aca agt ttt ctc tct gct gca tca 1535
 Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser
 500 505 510
 act gca atc tat gtt tac atg tat tcc ttt tac tac tat ttt ttc aaa 1583
 Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys
 515 520 525

aca aag atg tat ggc tta ttt caa aca tca ttt tac ttt gga tat atg 1631
 Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met
 530 535 540

gcg gta ttt agc aca gcc ttg ggg ata atg tgt gga gcg att ggt tac 1679
 Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr
 545 550 555

atg gga aca agt gcc ttt gtc cga aaa atc tat act aat gtg aaa att 1727
 Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile
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<400> 14

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 35 40 45

Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His
 50 55 60

Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly
 65 70 75 80

Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu
 85 90 95

Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys
 100 105 110

Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly
 115 120 125

BH
Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr
130 135 140

Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val
145 150 155 160

Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys Ile
165 170 175

Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe Glu
180 185 190

Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg Ile
195 200 205

His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Val
210 215 220

Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala
225 230 235 240

Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly
245 250 255

Sub
C1
Cont
Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro Ser
260 265 270

Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile
275 280 285

Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu
290 295 300

Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala
305 310 315 320

Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg
325 330 335

Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu
340 345 350

Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala
355 360 365

Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val Ala
370 375 380

Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val Gly
385 390 395 400

Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg
405 410 415

Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met Glu
420 425 430

Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile
435 440 445

Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile
450 455 460

Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile
465 470 475 480

Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala
485 490 495

Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr
500 505 510

Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr
515 520 525

Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala
530 535 540

Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met
545 550 555 560

Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp
565 570 575